

SEQUENCE LISTING

#4

<110> Lanes, Olav
 Willasen, Nils Peder
 Guddal, Per Henrik
 Gjellesvik, Dag Rune

<120> Cod uracil-DNA glycosylase, gene coding therefore, recombinant DNA containing said gene or operative parts thereof, a method for preparing said protein and the use of said protein or said operative pa

<130> U013209-3

<140> 09/758,017

<141> 2001-01-10

<150> 2000 5428

<151> 2000-10-27

<150> 2000 0163

<151> 2000-01-12

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<170> PatentIn Ver. 2.0

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Ile Ser Ser Asn Arg Xaa Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu

15 20 25

tgt ttt tct aaa tta atg aag ata acg ccg aag aaa ctg agg tcc tca 146 Cys Phe Ser Lys Leu Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser 30 35 40

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_	-	atg Met										242
		acg Thr										290
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		agg Arg 110										386
_	_	aca Thr										434
		gac Asp										482
		caa Gln										530
	_	ttg Leu	_	Thr	Asp	Asp	Gly	Phe				578
_		agc Ser 190										626
_		gtg Val										674
		ttc Phe										722

gga gtc gtt ttc Gly Val Val Phe			Ala His Lys	3 33. 3.3	70
acc atc gac agg of Thr Ile Asp Arg 2					18
cct ttg tct gct of Pro Leu Ser Ala 1					66
gct aac ggg ctg d Ala Asn Gly Leu 2 285					14
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Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys 35 40 45

Thr	Ser 50	Ser	Pro	Gln	Leu	Ser 55	Val	Glu	Gln	Leu	Glu 60	Arg	Met	Ala	Lys
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Gly	Phe	Gly	Glu	Thr 85	Trp	Arg	Arg	Glu	Leu 90	Ala	Ala	Glu	Phe	Glu 95	Lys
Pro	Tyr	Phe	Lys 100	Gln	Leu	Met	Ser	Phe 105	Val	Ala	Asp	Glu	Arg	Ser	Arg
His	Thr	Val 115	Tyr	Pro	Pro	Ala	Asp 120	Gln	Val	Tyr	Ser	Ser 125	Thr	Glu	Met
Cys	Asp 130	Ile	Gln	Asp	Val	Lys 135	Val	Val	Ile	Leu	Gly 140	GÌn	Asp	Pro	Tyr
His 145	Gly	Pro	Asn	Gln	Ala 150	His	Gly	Leu	Cys	Phe 155	Ser	Val	Gln	Lys	Pro 160
Val	Pro	Pro	Pro	Pro 165	Ser	Leu	Val	Asn	Ile 170	Tyr	Lys	Glu	Leu	Cys 175	Thr
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Ala	Lys	Gln 195	Gly	Val	Leu	Leu	Leu 200	Asn	Ala	Val	Leu	Thr 205	Val	Arg	Ala
His	Gln 210	Ala	Asn	Ser	His	Lys 215	Asp	Arg	Gly	Trp	Glu 220	Thr	Phe	Thr	Asp
	Val	Ile	Lys	Trp		Ser	Val	Asn	Arg	Glu 235	Gly	Val	Val	Phe	Leu 240
225					230					233					240

Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys 245 250 255

Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His 260 265 270

Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu 275 280 285

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gatggtttag gaggatagta ctttgacact ggttagcgaa ggggaaaacg gagttattgt 60 gcatatcgtt ttagccctac gtttaaaaa atg att ggt caa cag cat atc aac 113 Met Ile Gly Gln Gln His Ile Asn 1 5 tct ttc ttc ttc tca cca gtt tca aaa aag ag gtt tca aag gaa tta ggt 161 Ser Phe Phe Ser Pro Val Ser Lys Lys Arg Val Ser Lys Glu Leu Gly 10 15 20 aaa acc gaa aag cat gcc gaa gaa gtt cag ata acg ccg aag aaa ctg 209 Lys Thr Glu Lys His Ala Glu Glu Val Gln Ile Thr Pro Lys Lys Leu 25 30 35 40 agg tcc tca aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg 257 Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val 45 50 55 gag cag ctg gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag 305 Glu Gln Leu Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys 60 65 70 att aga gca aaa gca acg cct gca ggt ttc gga gag act tgg aga aga 353 Tle Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg 75 80 85 gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc 401 Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser 90 95 100 ttt gta gct gat gag agg acc cgt cac acc gtc tac cca ccg gct gat 449 Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp 105 110 120 caa gtg tac agt tgg aca gag att tgg aca att caa gtg ag agt 347 497					. (99	2)												
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gcatatcgtt ttagccctac gtttaaaaa atg att ggt caa cag cat atc aac 113 Met Ile Gly Gln Gln His Ile Asn 1																		
Met Ile Gly Gln Gln His Ile Asn 1	gat	ggt	tt	ag	gagg	atag	ta c	tttga	acact	t gg1	ttago	cgaa	ggg	gaaaa	acg o	gagt	tattgt	60
Met Ile Gly Gln Gln His Ile Asn 1	aca:	tat	cc	1++	ttaq	ccct	ദേ വ	httaa	aaaa	atα	att	aat	caa	caq	cat	atc	aac	113
tet tte tte tte tee tee ege get tee eas and eag aga get tee eas ged et tee eas eag gas et tee ged get ee eas eag ege et tee eas eag ege et tee eas eag ege et tee eas eag ege ege ege ege ege ege ege ege ege	gea		9	,														
Ser Phe Ne Phe 10 Ser Pro Val 15 Lys Lys Arg Val Ser Lys Code												··						
Ser Phe Ne Phe 10 Ser Pro Val 15 Lys Lys Arg Val Ser Lys Code																		
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aaa acc gaa acg cat gac gaa gaa gtt cag ata acg ccg aag aca ctg 209 Lys Thr Glu Lys His Ala Glu Glu Val Gln Ile Thr Pro Lys Lys Leu 30 agg tcc tca aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg 257 Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val 55 gag cag ctg gaa aga atg gcc aaa aat aat aag aca acg ccg ctg gac aag atg gcc aaa aat aag aca acg gcg ctt gac aag acg gcg ctg gcg cag cag cag cag cag cag cag cag ca	Ser	Ph	e	Phe	Ser	Pro	Val	Ser	Lys	Lys	Arg	Val	Ser	Lys	Glu	Leu	Gly	
Lys Thr Glu Lys His Ala Glu Glu Val Gln Ile Thr Pro Lys Lys Leu agg tcc tca aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg 257 Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val gag cag ctg gaa atg gcc aaa aat aag aag acg ctt gac aag 305 Glu Gln Leu Glu Arg Met Ala Lys Asn Lys Ala Ala Leu Asp Lys 60 60 65 70 <td></td> <td>1</td> <td>0</td> <td></td> <td></td> <td></td> <td></td> <td>15</td> <td></td> <td></td> <td></td> <td></td> <td>20</td> <td></td> <td></td> <td></td> <td></td> <td></td>		1	0					15					20					
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25																		209
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Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val 45	25						30					33					40	
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Glu Gln Leu Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys 60 65 70 att aga gca aaa gca acg cct gca ggt ttc gga gag act tgg aga aga 353 Ile Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg 75 80 85 gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc 401 Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser 90 95 100 ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat 449 Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp 105 110 115 120 caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497																		
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The Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg 75 80 85 gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc 401 Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser 90 95 100 ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat 449 Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp 105 110 115 120 caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497					60					65					70			
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gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc 401 Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser 90 95 100 ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat 449 Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp 105 110 115 120 caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497																		
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Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser 90 95 100 100 100 100 100 100 100 100 100 10				. 3										_				
Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser 90 95 100 100 100 100 100 100 100 100 100 10	gag	ct	g	gct	gca	gag	ttt	gaa	aag	cca	tac	ttc	aaa	caa	ttg	atg	tcc	401
ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp 110 115 120 caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497																		
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105 110 115 120 caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497		_		-	_													449
caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497			Τ	Ala	Asp	GLu		ser	Arg	HIS	Thr		Tyr	rro	rro	нта		
	102						110					113					120	
	caa	αt	a	tac	ant	taa	aca	gag	atσ	tat	gac	att	caa	gat	ata	aaa	gta	497

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				125					130					135		
				_	_			cac His 145					-			545
	_							gtt Val					Ser			593
				_	_	-		gac Asp								641
			_					gca Ala								689
		_	_				-	cat His	_	_				_	_	737
								gct Ala 225								785
		-						ttc Phe								833
								cgt Arg								881
				_		_		cgt								929
His 265	Pro	Ser	Pro	Leu	Ser 270	Ala	His	Arg	GŢĀ	Phe 275	Leu	GLY	Cys	Lys	His 280	
								aaa Lys		Ser						977
aac	tgg	aga	gca	ctc	taac	ctctt	ta t	gcto	gcctt	a ta	actgt	taac	c tgt	ttta	aga	1032

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Asn Trp Arg Ala Leu

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Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
50 55 60

Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala 65 70 75 80

Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
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Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg 100 105 110

His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Trp Thr Glu Met
115 120 125

Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr 130 135 140

His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro 145 150 155 160

Val Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr

165 170 175

Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp 180 185 190

Ala Asn Lys Gly Cys Cys Cys Leu Thr Arg Cys Leu Thr Val Arg Ala 195 200 205

His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Ser Thr Asp 210 215 220

Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu 225 230 235 240

Phe Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys 245 250 255

Arg His His Val Leu Gln Ala Leu His Pro Ser Pro Leu Ser Ala His 260 265 270

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Sequence - Primer used to prepare cDNA of a fragment of UNG gene

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